

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 101643,836  
Source: \_\_\_\_\_  
Date Processed by STIC: \_\_\_\_\_

***ENTERED***



IFWO

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION: US/10/643,836**

**DATE: 01/11/2005**  
**TIME: 12:22:35**

**Input Set : N:\Crf3\RULE60\10643836.RAW.txt**  
**Output Set: N:\CRF4\01112005\J643836.raw**

1 <110> APPLICANT: Dumas Milne Edwards, Jean Baptiste  
 2 Bougueleret, Lydie  
 3 Jobert, Severin  
 4 <120> TITLE OF INVENTION: FULL-LENGTH HUMAN cDNAs ENCODING POTENTIALLY SECRETED  
 PROTEINS  
 5 <130> FILE REFERENCE: 78.US3.REG  
 6 <140> CURRENT APPLICATION NUMBER: 10/643,836  
 7 <141> CURRENT FILING DATE: 2003-08-19  
 8 <150> PRIOR APPLICATION NUMBER: US/09/731,872  
 9 <151> PRIOR FILING DATE: 2000-12-07  
 10 <150> PRIOR APPLICATION NUMBER: US 60/169,629  
 11 <151> PRIOR FILING DATE: 1999-12-08  
 12 <150> PRIOR APPLICATION NUMBER: US 60/187,470  
 13 <151> PRIOR FILING DATE: 2000-03-06  
 14 <160> NUMBER OF SEQ ID NOS: 482  
 15 <170> SOFTWARE: Patent.pm  
 17 <210> SEQ ID NO: 1  
 18 <211> LENGTH: 2201  
 19 <212> TYPE: DNA  
 20 <213> ORGANISM: Homo sapiens  
 21 <220> FEATURE:  
 22 <221> NAME/KEY: CDS  
 23 <222> LOCATION: 169..1692  
 24 <221> NAME/KEY: sig\_peptide  
 25 <222> LOCATION: 169..249  
 26 <223> OTHER INFORMATION: Von Heijne matrix  
 27 score 7.15265901862021  
 28 seq VLLLLLLEERGMFS/SP  
 W--> 29 <400> 1  
 30 agatgtgaat agtccacta taccaggctc gtcttccttc cgggggacaaa cgtgggtcag 60  
 31 ggcacagaga gatatttaat gtcaccctct tggggcttcc atgggactcc ctctgccac 120  
 32 tttttggag gttgggaaag ttgcttagagg cttcagaact ccagccta atg gat ccc 177  
 33 Met Asp Pro  
 34 -25  
 35 aaa ctc ggg aga atg gct gcg tcc ctg gct gtg ctg ctg ctg 225  
 36 Lys Leu Gly Arg Met Ala Ala Ser Leu Leu Ala Val Leu Leu Leu  
 37 -20 -15 -10  
 38 ctg ctg gag cgc ggc atg ttc tcc tca ccc tcc ccg ccc ccg gcg ctg 273  
 39 Leu Leu Glu Arg Gly Met Phe Ser Ser Pro Ser Pro Pro Ala Leu  
 40 -5 1 5  
 41 tta gag aaa gtc ttc cag tac att gac ctc cat cag gat gaa ttt gtg 321  
 42 Leu Glu Lys Val Phe Gln Tyr Ile Asp Leu His Gln Asp Glu Phe Val  
 43 10 15 20  
 44 cag acg ctg aag gag tgg gtg gcc atc gag agc gac tct gtc cag cct 369

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Output Set: N:\CRF4\01112005\J643836.raw

45	Gln Thr Leu Lys Glu Trp Val Ala Ile Glu Ser Asp Ser Val Gln Pro		
46	25 30 35 40		
47	gtg cct cgc ttc aga caa gag ctc ttc aga atg atg gcc gtg gct gcg	417	
48	Val Pro Arg Phe Arg Gln Glu Leu Phe Arg Met Met Ala Val Ala Ala		
49	45 50 55		
50	gac acg ctg cag cgc ctg ggg gcc cgt gtg gcc tcg gtg gac atg ggt	465	
51	Asp Thr Leu Gln Arg Leu Gly Ala Arg Val Ala Ser Val Asp Met Gly		
52	60 65 70		
53	cct cag cag ctg ccc gat ggt cag agt ctt cca ata cct ccc gtc atc	513	
54	Pro Gln Gln Leu Pro Asp Gly Gln Ser Leu Pro Ile Pro Pro Val Ile		
55	75 80 85		
56	ctg gcc gaa ctg ggg agc gat ccc acg aaa ggc acc gtg tgc ttc tac	561	
57	Leu Ala Glu Leu Gly Ser Asp Pro Thr Lys Gly Thr Val Cys Phe Tyr		
58	90 95 100		
59	ggc cac ttg gac gtg cag ctc gct gac cgg ggc gat ggg tgg ctc acg	609	
60	Gly His Leu Asp Val Gln Pro Ala Asp Arg Gly Asp Gly Trp Leu Thr		
61	105 110 115 120		
62	gac ccc tat gtg ctg acg gag gta gac ggg aaa ctt tat gga cga gga	657	
63	Asp Pro Tyr Val Leu Thr Glu Val Asp Gly Lys Leu Tyr Gly Arg Gly		
64	125 130 135		
65	gcg acc gac aac aaa ggc cct gtc ttg gct tgg atc aat gct gtg agc	705	
66	Ala Thr Asp Asn Lys Gly Pro Val Leu Ala Trp Ile Asn Ala Val Ser		
67	140 145 150		
68	gcc ttc aga gcc ctg gag caa gat ctt cct gtg aat atc aaa ttc atc	753	
69	Ala Phe Arg Ala Leu Glu Gln Asp Leu Pro Val Asn Ile Lys Phe Ile		
70	155 160 165		
71	att gag ggg atg gaa gag gct ggc tct gtt gcc ctg gag gaa ctt gtg	801	
72	Ile Glu Gly Met Glu Glu Ala Gly Ser Val Ala Leu Glu Glu Leu Val		
73	170 175 180		
74	gaa aaa gaa aag gac cga ttc ttc tct ggt gtg gac tac att gta att	849	
75	Glu Lys Glu Lys Asp Arg Phe Phe Ser Gly Val Asp Tyr Ile Val Ile		
76	185 190 195 200		
77	tca gat aac ctg tgg atc agc caa agg aag cca gca atc act tat gga	897	
78	Ser Asp Asn Leu Trp Ile Ser Gln Arg Lys Pro Ala Ile Thr Tyr Gly		
79	205 210 215		
80	acc cgg ggg aac agc tac ttc atg gtg gag gtg aaa tgc aga gac cag	945	
81	Thr Arg Gly Asn Ser Tyr Phe Met Val Glu Val Lys Cys Arg Asp Gln		
82	220 225 230		
83	gat ttt cac tca gga acc ttt ggt ggc atc ctt cat gaa cca atg gct	993	
84	Asp Phe His Ser Gly Thr Phe Gly Gly Ile Leu His Glu Pro Met Ala		
85	235 240 245		
86	gat ctg gtt gct ctt ctc ggt agc ctg gta gac tcg tct ggt cat atc	1041	
87	Asp Leu Val Ala Leu Leu Gly Ser Leu Val Asp Ser Ser Gly His Ile		
88	250 255 260		
89	ctg gtc cct gga atc tat gat gaa gtg gtt cct ctt aca gaa gag gaa	1089	
90	Leu Val Pro Gly Ile Tyr Asp Glu Val Val Pro Leu Thr Glu Glu Glu		
91	265 270 275 280		
92	ata aat aca tac aaa gcc atc cat cta gac cta gaa gaa tac cgg aat	1137	
93	Ile Asn Thr Tyr Lys Ala Ile His Leu Asp Leu Glu Glu Tyr Arg Asn		

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94	285	290	295	
95	agc agc cgg gtt gag aaa ttt ctg ttc gat act aag gag gag att cta			1185
96	Ser Ser Arg Val Glu Lys Phe Leu Phe Asp Thr Lys Glu Glu Ile Leu			
97	300	305	310	
98	atg cac ctc tgg agg tac cca tct ctt tct att cat ggg atc gag ggc			1233
99	Met His Leu Trp Arg Tyr Pro Ser Leu Ser Ile His Gly Ile Glu Gly			
100	315	320	325	
101	gcg ttt gat gag cct gga act aaa aca gtc ata cct ggc cga gtt ata			1281
102	Ala Phe Asp Glu Pro Gly Thr Lys Thr Val Ile Pro Gly Arg Val Ile			
103	330	335	340	
104	gga aaa ttt tca atc cgt cta gtc cct cac atg aat gtg tct gcg gtg			1329
105	Gly Lys Phe Ser Ile Arg Leu Val Pro His Met Asn Val Ser Ala Val			
106	345	350	355	360
107	gaa aaa cag gtg aca cga cat ctt gaa gat gtg ttc tcc aaa aga aat			1377
108	Glu Lys Gln Val Thr Arg His Leu Glu Asp Val Phe Ser Lys Arg Asn			
109	365	370	375	
110	agt tcc aac aag atg gtt tcc atg act cta gga cta cac ccg tgg			1425
111	Ser Ser Asn Lys Met Val Val Ser Met Thr Leu Gly Leu His Pro Trp			
112	380	385	390	
113	att gca aat att gat gac acc cag tat ctc gca gca aaa aga gcg atc			1473
114	Ile Ala Asn Ile Asp Asp Thr Gln Tyr Leu Ala Ala Lys Arg Ala Ile			
115	395	400	405	
116	aga aca gtg ttt gga aca gaa cca gat atg atc ccg gat gga tcc acc			1521
117	Arg Thr Val Phe Gly Thr Glu Pro Asp Met Ile Arg Asp Gly Ser Thr			
118	410	415	420	
119	att cca att gcc aaa atg ttc cag gag atc gtc cac aag agc gtg gtg			1569
120	Ile Pro Ile Ala Lys Met Phe Gln Glu Ile Val His Lys Ser Val Val			
121	425	430	435	440
122	cta att ccg ctg gga gct gtt gat gat gga gaa cat tcg cag aat gag			1617
123	Leu Ile Pro Leu Gly Ala Val Asp Asp Gly Glu His Ser Gln Asn Glu			
124	445	450	455	
125	aaa atc aac agg tgg aac tac ata gag gga acc aaa tta ttt gct gcc			1665
126	Lys Ile Asn Arg Trp Asn Tyr Ile Glu Gly Thr Lys Leu Phe Ala Ala			
127	460	465	470	
128	ttt ttc tta gag atg gcc cag ctc cat taatcacaag aaccttctag			1712
129	Phe Phe Leu Glu Met Ala Gln Leu His			
130	475	480		
131	tctgatctga tccactgaca gattcacctc ccccacatcc ctagacaggg atgaaatgt			1772
132	aatatccaga gaatttgggt ctatgtatgt acatttcccc ttccatttaa aatgtcttgg			1832
133	gatatctgga tcagtaataa aatatttcaa aggacacatg gttggaaatg gtttaaggtc			1892
134	cccccactgca caccttcctc aagtcatagc tgcttcagc aacttgattt ccccaagtcc			1952
135	tgtgcaatag ccccgaggatt ggattccttc caaccttta gcatatctcc aaccttgc当地			2012
136	tttgattggc ataatcaactc cagtttgctt tcttaggtctt caagtgc当地 tgacacataa			2072
137	tcattccatc caatgatcgc ctttgc当地 ccacttcc ttatctt attaataaaaa			2132
138	atgttggctt ccaccactga aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaagaaaaaaaaa			2192
139	aaaaaaaaaa			2201
141	<210> SEQ ID NO: 2			
142	<211> LENGTH: 1631			
143	<212> TYPE: DNA			

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Output Set: N:\CRF4\01112005\J643836.raw

144 <213> ORGANISM: Homo sapiens  
145 <220> FEATURE:  
146 <221> NAME/KEY: CDS  
147 <222> LOCATION: 148..1140  
148 <221> NAME/KEY: sig\_peptide  
149 <222> LOCATION: 148..240  
150 <223> OTHER INFORMATION: Von Heijne matrix  
151 score 10.0910253445132  
152 seq LVLLVTRSPVNA/CL  
W--> 153 <400> 2  
154 gtcgtgtgcc gccattgtgc ggcgctggtc ccctcagagg gttcctgctg ctgcgggtgc 60  
155 cttggaccct cccccctcgct ttcgttcta ctgccccagg agccccgggg gtccgggact 120  
156 cccgtccgtg ccgggtgcggg cgccggc atg tgg ctg tgg gag gac cag ggc ggc 174  
157 Met Trp Leu Trp Glu Asp Gln Gly Gly  
158 -30 -25  
159 ctc ctg ggc cct ttc tcc ctg ctg cta gtg ctg ctg ctg gtg acg 222  
160 Leu Leu Gly Pro Phe Ser Phe Leu Leu Leu Val Leu Leu Val Thr  
161 -20 -15 -10  
162 cggtgcggtc aat gcc tgc ctc ctc acc ggc acg ctc ttc gtt cta 270  
163 Arg Ser Pro Val Asn Ala Cys Leu Leu Thr Gly Ser Leu Phe Val Leu  
164 -5 1 5 10  
165 ctgcgtc ttc agc ttt gag ccg gtg ccc tct tgc agg gcc ctg cag 318  
166 Leu Arg Val Phe Ser Phe Glu Pro Val Pro Ser Cys Arg Ala Leu Gln  
167 15 20 25  
168 gtgcgtc aag ccc ccg gac cgc att tct gcc atc gcc cac cgt ggc ggc 366  
169 Val Leu Lys Pro Arg Asp Arg Ile Ser Ala Ile Ala His Arg Gly Gly  
170 30 35 40  
171 agc cac gac gcg ccc gag aac acg ctg gcg gcc att cgg cag gca gct 414  
172 Ser His Asp Ala Pro Glu Asn Thr Leu Ala Ala Ile Arg Gln Ala Ala  
173 45 50 55  
174 aag aat gga gca aca ggc gtg gag ttg gac att gag ttt act tct gac 462  
175 Lys Asn Gly Ala Thr Gly Val Glu Leu Asp Ile Glu Phe Thr Ser Asp  
176 60 65 70  
177 ggg att cct gtc tta atg cac gat aac aca gta gat agg acg act gat 510  
178 Gly Ile Pro Val Leu Met His Asp Asn Thr Val Asp Arg Thr Thr Asp  
179 75 80 85 90  
180 ggg act ggg cga ttg tgt gat ttg aca ttt gaa caa att agg aag ctg 558  
181 Gly Thr Gly Arg Leu Cys Asp Leu Thr Phe Glu Gln Ile Arg Lys Leu  
182 95 100 105  
183 aat cct gca gca aac cac aga ctc agg aat gat ttc cct gat gaa aag 606  
184 Asn Pro Ala Ala Asn His Arg Leu Arg Asn Asp Phe Pro Asp Glu Lys  
185 110 115 120  
186 atc cct acc cta atg gaa gct gtt gca gag tgc cta aac cat aac ctc 654  
187 Ile Pro Thr Leu Met Glu Ala Val Ala Glu Cys Leu Asn His Asn Leu  
188 125 130 135  
189 aca atc ttc ttt gat gtc aaa ggc cat gca cac aag gct act gag gct 702  
190 Thr Ile Phe Phe Asp Val Lys Gly His Ala His Lys Ala Thr Glu Ala  
191 140 145 150  
192 cta aag aaa atg tat atg gaa ttt cct caa ctg tat aat aat agt gtg 750

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193	Leu Lys Lys Met Tyr Met Glu Phe Pro Gln Leu Tyr Asn Asn Ser Val	
194	155 160 165 170	
195	gtc tgt tct ttc ttg cca gaa gtt atc tac aag atg aga caa aca gat	798
196	Val Cys Ser Phe Leu Pro Glu Val Ile Tyr Lys Met Arg Gln Thr Asp	
197	175 180 185	
198	cgg gat gta ata aca gca tta act cac aga cct tgg agc cta agc cat	846
199	Arg Asp Val Ile Thr Ala Leu Thr His Arg Pro Trp Ser Leu Ser His	
200	190 195 200	
201	aca gga gat ggg aaa cca cgc tat gat act ttc tgg aaa cat ttt ata	894
202	Thr Gly Asp Gly Lys Pro Arg Tyr Asp Thr Phe Trp Lys His Phe Ile	
203	205 210 215	
204	ttt gtt atg atg gac att ttg ctc gat tgg agc atg cat aat atc ttg	942
205	Phe Val Met Met Asp Ile Leu Leu Asp Trp Ser Met His Asn Ile Leu	
206	220 225 230	
207	tgg tac ctg tgt gga att tca gct ttc ctc atg caa aag gat ttt gta	990
208	Trp Tyr Leu Cys Gly Ile Ser Ala Phe Leu Met Gln Lys Asp Phe Val	
209	235 240 245 250	
210	tcc ccg gcc tac ttg aag aag tgg tca gct aaa gga atc cag gtt gtt	1038
211	Ser Pro Ala Tyr Leu Lys Trp Ser Ala Lys Gly Ile Gln Val Val	
212	255 260 265	
213	ggt tgg act gtt aat acc ttt gat gaa aag agt tac tac gaa tcc cat	1086
214	Gly Trp Thr Val Asn Thr Phe Asp Glu Lys Ser Tyr Tyr Glu Ser His	
215	270 275 280	
216	ctt ggt tcc agc tat atc act gac agc atg gta gaa gac tgc gaa cct	1134
217	Leu Gly Ser Ser Tyr Ile Thr Asp Ser Met Val Glu Asp Cys Glu Pro.	
218	285 290 295	
219	cac ttc tagactttca cggtggacg aaacgggttc agaaaactgcc aggggcctca	1190
220	His Phe	
221	300	
222	tacaggata tcaaaatacc ctttgtcta gcccaggccc tggggaatca ggtgactcac	1250
223	acaaaatgcaa tagttggtca ctgcattttt acctgaacca aagctaaacc cgggtttgcc	1310
224	accatgcacc atggcatgcc agagttcaac actgttgctc ttgaaaatct ggggtctgaa	1370
225	aaaacgcaca agagccctg ccctgcccta gctgaggcac acagggagac ccagtgagga	1430
226	taagcacaga ttgaattgta caatttgcag atgcagatgt aaatgcattgg gacatgcattg	1490
227	ataactcaga gttgacattt taaaacttgc cacacttatt tcaaatattt gtactcagct	1550
228	atgtaacat gtactgtaga catcaaactt gtggccatac taataaaatt attaaaagga	1610
229	gcacaaaaaa aaaaaaaaaa a	1631
231	<210> SEQ ID NO: 3	
232	<211> LENGTH: 1245	
233	<212> TYPE: DNA	
234	<213> ORGANISM: Homo sapiens	
235	<220> FEATURE:	
236	<221> NAME/KEY: CDS	
237	<222> LOCATION: 85..906	
238	<221> NAME/KEY: sig_peptide	
239	<222> LOCATION: 85..135	
240	<223> OTHER INFORMATION: Von Heijne matrix	
241	score 3.86022363031904	
242	seq GFVAALVAGGVAG/VS	

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 01/11/2005  
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**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:12; Xaa Pos. 44,45  
Seq#:20; N Pos. 989  
Seq#:45; Xaa Pos. 132  
Seq#:97; Xaa Pos. 21  
Seq#:103; Xaa Pos. 185  
Seq#:104; N Pos. 972  
Seq#:115; Xaa Pos. 41  
Seq#:135; N Pos. 347  
Seq#:135; Xaa Pos. 47  
Seq#:137; Xaa Pos. 50,51  
Seq#:165; N Pos. 1707  
Seq#:188; N Pos. 871  
Seq#:202; N Pos. 483  
Seq#:207; Xaa Pos. 113,114,115  
Seq#:210; Xaa Pos. 76  
Seq#:220; Xaa Pos. 95  
Seq#:253; Xaa Pos. 44,45  
Seq#:286; Xaa Pos. 132  
Seq#:338; Xaa Pos. 21  
Seq#:344; Xaa Pos. 185  
Seq#:356; Xaa Pos. 41  
Seq#:376; Xaa Pos. 47  
Seq#:378; Xaa Pos. 50,51  
Seq#:448; Xaa Pos. 113,114,115  
Seq#:451; Xaa Pos. 76  
Seq#:461; Xaa Pos. 95

### Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 4

## VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10643836.RAW.txt  
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L:29 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1  
L:153 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2  
L:243 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3  
L:318 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4  
L:417 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5  
L:460 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6  
L:551 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7  
L:650 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8  
L:747 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9  
L:794 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:10  
L:850 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11  
L:896 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12  
L:915 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:412  
L:956 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13  
L:1005 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:14  
L:1104 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:15  
L:1170 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:16  
L:1238 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:17  
L:1293 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:18  
L:1396 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:19  
L:1446 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20  
L:1449 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:20  
L:1499 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:966  
L:1516 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:21  
L:1549 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:22  
L:1589 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:23  
L:1641 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:24  
L:1679 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:25  
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L:1896 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:29  
L:1931 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30  
L:2046 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:31  
L:2142 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:33  
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L:2340 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:36  
L:2425 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:37  
L:2547 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:38  
L:2621 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:39  
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L:2770 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:41  
L:2893 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:42  
L:3002 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:43  
L:3106 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:44  
L:3191 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:45  
L:3225 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:654

## VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10643836.RAW.txt  
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L:3298 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:46  
L:3384 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:47  
L:3481 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:48  
L:3529 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:49  
L:3572 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:50  
L:6456 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:97 after pos.:144  
L:6752 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:103 after pos.:923  
L:6821 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:104 after pos.:935  
L:7430 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:115 after pos.:369  
L:8386 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:135 after pos.:310  
M:341 Repeated in SeqNo=135  
L:8471 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:137 after pos.:253  
M:341 Repeated in SeqNo=137  
L:10269 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:165 after pos.:1691  
L:11620 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:188 after pos.:830  
L:12113 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:202 after pos.:465  
L:12300 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:207 after pos.:445  
L:12472 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:210 after pos.:352  
L:13039 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:220 after pos.:402  
L:14556 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:253 after pos.:64  
L:15877 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:286 after pos.:144  
L:17668 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:338 after pos.:32  
L:17827 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:344 after pos.:192  
L:18185 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:356 after pos.:64  
L:18728 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:376 after pos.:64  
L:18780 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:378 after pos.:48  
M:341 Repeated in SeqNo=378  
L:20843 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:448 after pos.:112  
L:20937 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:451 after pos.:64  
L:21264 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:461 after pos.:80